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RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/505,316

TIME: 16:10:16

Input Set : D:\1242-50-3 PCT-US.ST25.txt

Output Set: N:\CRF4\08262004\J505316.raw

3 <110> APPLICANT: Vanderbilt University
 4 Case Western Reserve University
 5 Mount, David B
 6 Romero, Michael
 8 <120> TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A7 and SLC26A9 ANION
 9 EXCHANGERS
 11 <130> FILE REFERENCE: 1242/50/3 PCT-US
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/505,316
 C--> 13 <141> CURRENT FILING DATE: 2004-08-20
 13 <150> PRIOR APPLICATION NUMBER: US 60/360,287
 14 <151> PRIOR FILING DATE: 2002-02-28
 16 <150> PRIOR APPLICATION NUMBER: PCT/US03/06220
 17 <151> PRIOR FILING DATE: 2003-02-28
 19 <160> NUMBER OF SEQ ID NOS: 33
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1971
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
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 31 tgtgaagaca ttatacagt gtgtagaagg cgactgccc ttttgattg ggcaccacat 120
 33 tacaatctga aagaaaactt gcttcagac actgtgtctg ggataatgtt ggcagttcaa 180
 35 caggtgacct aaggattggc ctttgcctgt ctctcatctg tgcacccagt gtttggttta 240
 37 tatgggtctc tgtttcctgc cataatttat gccatatgtt gaatgggaca tcatgttgcc 300
 39 acaggcacct ttgccttgac atccttaata tcagccaacg ccgtggaacg gattgtccct 360
 41 cagaacatgc agaactctac cacacagagt aacacaagcg tgctgggctt atccgacttt 420
 43 gaaatgcaaa ggatccacgt tgcctgcagc gtttccttct tgggaggtgt gattcagggtg 480
 45 gccatgtttg tgcctgcaact gggcagtgcc acatttgttg tcacagagcc tgtgatcagc 540
 47 gcaatgacaa ctggggctgc caccatgtg gtgacttcac aagtcaaata tctcttgga 600
 49 atgaaaatgc catatatatc cggaccactt ggattctttt atatttatgc atatgttttt 660
 51 gaaaacatca agtctgtgag actggaagca ttgcttttat ccttgctgag cattgtggtc 720
 53 cttgttcttg ttaaagagct gaatgaacag tttaaaagga aaattaaagt tgttcttct 780
 55 gtagatttag ttttgattat tgcctgcatc tttgcttggt attgcaccaa tatggaaaac 840
 57 acatatggat tagaagtagt tgggtcatatt ccacaaggaa ttccctcacc tagagctccc 900
 59 ccgatgaaca tcctctctgc ggtgatcact gaagctttcg gagtggaact tgtaggctat 960
 61 gtggcctcac tggctcttgc tcaaggatct gccaaaaaat tcaaatatte aattgatgac 1020
 63 aaccaggaaat ttttgcccca tggcctcagc aatatagttt ctccattttt cttctgcata 1080
 65 ccaagtgtct ctgccatggg aaggacggct ggctgtaca gcacaggagc gaagacacag 1140
 67 gtggcttgct taatatcttg cattttcgtc cttatagtca tctatgcaat aggaccttg 1200
 69 ctttactggc tgcctatgtg tgccttgca agcattattg ttgtgggact gaagggaatg 1260
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75 gttgttttga ccatagctat agtgatagga cgcttcccaa gagcaatgac tgtaagtata 1440
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79 caggtgaaaa ttatctcaat aaacaacccg cttgttttcc tgaatgcaaa aaaattttat 1560
81 actgatttaa tgaacatgat ccaaaaggaa aatgcctgta atcagccact tgatgatatc 1620
83 agcaagtgtg aacaaaacac attgcttaat tccctatcca atggcaactg caatgaagaa 1680
85 gcttcacagt cctgccctaa tgagaagtgt tatttaatcc tggattgcag tggatttacc 1740
87 ttttttgact attctggagt ctccatgctt gttgaggttt acatggactg taaaggcagg 1800
89 agtgtggatg tattgttagc ccattgtaca gcttccttga taaaagcaat gacgtattat 1860
91 ggaaacctag actcagagaa accaattttt tttgaatcgg tatctgctgc aataagtcac 1920
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97 <211> LENGTH: 656
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111 Pro Ile Leu Glu Trp Ala Pro Gln Tyr Asn Leu Lys Glu Asn Leu Leu
112 35 40 45
115 Pro Asp Thr Val Ser Gly Ile Met Leu Ala Val Gln Gln Val Ala Gln
116 50 55 60
119 Gly Leu Ser Phe Ala Met Leu Ser Ser Val His Pro Val Phe Gly Leu
120 65 70 75 80
123 Tyr Gly Ser Leu Phe Pro Ala Ile Ile Tyr Ala Ile Phe Gly Met Gly
124 85 90 95
127 Arg His Val Ala Thr Gly Thr Phe Ala Leu Thr Ser Leu Ile Ser Ala
128 100 105 110
131 Asn Ala Val Glu Arg Leu Val Pro Gln Ser Ser Arg Asn Leu Thr Thr
132 115 120 125
135 Gln Ser Asn Ser Ser Val Leu Gly Leu Ser Glu Phe Glu Leu Gln Arg
136 130 135 140
139 Ile Gly Val Ala Ala Ala Val Ser Phe Leu Gly Gly Val Ile Gln Leu
140 145 150 155 160
143 Val Met Phe Val Leu Gln Leu Gly Ser Ala Thr Phe Leu Leu Thr Glu
144 165 170 175
147 Pro Val Ile Ser Ala Met Thr Thr Gly Ala Ala Thr His Val Val Thr
148 180 185 190
151 Ser Gln Val Lys Tyr Leu Leu Gly Ile Lys Met Pro Tyr Ile Ser Gly
152 195 200 205
155 Pro Leu Gly Phe Phe Tyr Ile Tyr Ala Tyr Val Phe Glu Asn Ile Lys
156 210 215 220
159 Ser Val Gln Leu Glu Ala Leu Leu Leu Ser Leu Leu Ser Ile Ile Val
160 225 230 235 240
163 Leu Val Leu Val Lys Glu Leu Asn Glu Gln Phe Lys Arg Lys Ile Lys
164 245 250 255
167 Val Val Leu Pro Val Asp Leu Val Leu Ile Ile Ala Ala Ser Phe Ala
168 260 265 270

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171 Cys Tyr Cys Thr Asn Met Glu Asn Thr Tyr Gly Leu Glu Val Val Gly
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175 His Ile Pro Asn Gly Ile Pro Pro Pro Arg Ala Pro Pro Met Asn Ile
176      290      295      300
179 Leu Ser Ala Val Leu Thr Glu Ala Phe Gly Val Ala Leu Val Gly Tyr
180 305      310      315      320
183 Val Ala Ser Leu Ala Leu Ala Gln Gly Ser Ala Lys Lys Phe Lys Tyr
184      325      330      335
187 Ser Val Asp Asp Asn Gln Glu Phe Leu Ala His Gly Leu Ser Asn Val
188      340      345      350
191 Ile Pro Ser Phe Leu Phe Cys Ile Pro Ser Ala Ala Ala Met Gly Arg
192      355      360      365
195 Thr Ala Gly Leu Tyr Ser Thr Gly Ala Lys Thr Gln Val Ala Cys Leu
196      370      375      380
199 Ile Ser Cys Ile Phe Val Leu Ile Val Ile Tyr Ala Ile Gly Pro Leu
200 385      390      395      400
203 Leu Tyr Trp Leu Pro Met Cys Val Leu Ala Ser Ile Ile Val Val Gly
204      405      410      415
207 Leu Lys Gly Met Leu Ile Gln Phe Arg Asp Leu Lys Lys Tyr Trp Asn
208      420      425      430
211 Val Asp Lys Ile Asp Trp Gly Ile Trp Ile Ser Thr Tyr Ile Phe Thr
212      435      440      445
215 Ile Cys Phe Ala Ala Asn Val Gly Leu Leu Phe Gly Val Ile Cys Thr
216      450      455      460
219 Ile Ala Ile Val Leu Gly Arg Phe Pro Arg Ala Lys Thr Leu Ser Ile
220 465      470      475      480
223 Thr Asp Met Lys Glu Met Glu Leu Lys Val Lys Thr Glu Met His Asp
224      485      490      495
227 Glu Thr Ser Gln Gln Ile Lys Ile Ile Ser Ile Asn Asn Pro Leu Val
228      500      505      510
231 Phe Leu Asn Ala Lys Lys Phe Ser Ala Asp Leu Met Lys Ile Ile Leu
232      515      520      525
235 Lys Glu Ser Asp Ser Asn Gln Pro Leu Asp Asp Val Ser Lys Cys Glu
236      530      535      540
239 Gln Asn Thr Leu Leu Ser Ser Leu Ser Asn Gly Asn Cys Asn Glu Glu
240 545      550      555      560
243 Ala Ser Gln Pro Cys Ser Ser Glu Lys Cys Ser Leu Val Leu Asn Cys
244      565      570      575
247 Ser Gly Leu Thr Phe Phe Asp Tyr Thr Gly Val Ser Thr Leu Val Glu
248      580      585      590
251 Leu Tyr Leu Asp Cys Lys Ser Arg Ser Val Asp Val Phe Leu Ala Asn
252      595      600      605
255 Cys Thr Ala Ser Leu Ile Lys Ala Met Thr Tyr Tyr Gly Asp Leu Asp
256      610      615      620
259 Thr Glu Lys Pro Ile Phe Phe Asp Ser Val Pro Ala Ala Ile Thr Ile
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263 Ile Gln Ser Asn Lys Asn Leu Ser Lys Ala Ser Asp His Ser Glu Val
264      645      650      655
267 <210> SEQ ID NO: 3

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268 <211> LENGTH: 2289
269 <212> TYPE: DNA
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277 ggcgcctacc tatcttgga tgggcaccgc agtacaatct gaaggaaaac ctgcttccag      180
279 aactgtgtgc tgggataatg ttggcagttc aacagggtggc acaagggtctg tcttctgcta      240
281 tgctttcatc tgtacacca gtttttggtt tatatggatc tctgtttcca gccatcattt      300
283 atgctatatt tggaatgggg cgccatggtt ccacaggcac ctttgccctt acatccttga      360
285 tatcagccaa cgctgtggaa cgactgggtc ctcagagcag caggaacctc accacacaga      420
287 gcaactcaag tgtgttgggc ttatccgagt ttgagctgca gagaatcggg gttgcagcgg      480
289 ctgtttcttt cttgggtgga gtgattcagc tgggtcatgt tgtgctgcag ctgggcagtg      540
291 ccacattcct gcttacagag cctgtgatca gcgccatgac cacagggggc gccacccatg      600
293 tctgtacatc acaagtcaag tatctcttgg gaatcaaaat gccatatata tccggaccac      660
295 tgggattctt ttatatatt gcgtatgtct ttgagaacat caagtctgtc cagctggaag      720
297 cactgctctt atctttgctg agcatcattg tccttgttct cgtaaagag ctgaatgaac      780
299 agtttaaaag aaaaattaaa gttgttcttc ctgtcgactt agttttgatc attgcccctt      840
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303 ttccaaacgg gattcctcct ccccggtgtc cccaatgaa catcctctct gcagtgtca      960
305 ctgaagcttt cggagttgca cttgtaggct atgtggcctc gctggctctc gcacaaggat     1020
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313 tccttattgt catctatgca ataggacctc tgctgtactg gctgcccatg tgcgttcttg     1260
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325 cacttgtttt cctgaatgca aagaaattta gtgctgattt gatgaaaata atcctaaagg     1620
327 aaagtgcagc caaccaacca cttgatgatg tcagcaagtg tgaacagaac accttgctca     1680
329 gttccctgtc caacggcaac tgcaatgaag aggcctccca gccctgctcc agcgagaagt     1740
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333 ttgttgagct ctaccttgat tgcaagagca ggagtgtgga tgtgttctta gccaaactgta     1860
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337 tttttgactc ggtacctgct gcgataacta tcatccaatc aaataagaat ttgagcaagg     1980
339 ccagtgacca cagtgaagtc tgagacccat gtgttgaaat gcacgcctca tctttagcag     2040
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352 <210> SEQ ID NO: 4
353 <211> LENGTH: 656
354 <212> TYPE: PRT
355 <213> ORGANISM: Mus musculus
357 <400> SEQUENCE: 4
359 Met Thr Gly Ala Lys Arg Lys Lys Arg Ser Val Leu Trp.Gly Lys Met

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368           35           40           45
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372           50           55           60
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376 65           70           75           80
379 Tyr Gly Ser Leu Phe Pro Ala Ile Ile Tyr Ala Ile Phe Gly Met Gly
380           85           90           95
383 Arg His Val Ala Thr Gly Thr Phe Ala Leu Thr Ser Leu Ile Ser Ala
384           100          105          110
387 Asn Ala Val Glu Arg Leu Val Pro Gln Ser Ser Arg Asn Leu Thr Thr
388           115          120          125
391 Gln Ser Asn Ser Ser Val Leu Gly Leu Ser Glu Phe Glu Leu Gln Arg
392           130          135          140
395 Ile Gly Val Ala Ala Ala Val Ser Phe Leu Gly Gly Val Ile Gln Leu
396 145          150          155          160
399 Val Met Phe Val Leu Gln Leu Gly Ser Ala Thr Phe Leu Leu Thr Glu
400           165          170          175
403 Pro Val Ile Ser Ala Met Thr Thr Gly Ala Ala Thr His Val Val Thr
404           180          185          190
407 Ser Gln Val Lys Tyr Leu Leu Gly Ile Lys Met Pro Tyr Ile Ser Gly
408           195          200          205
411 Pro Leu Gly Phe Phe Tyr Ile Tyr Ala Tyr Val Phe Glu Asn Ile Lys
412           210          215          220
415 Ser Val Gln Leu Glu Ala Leu Leu Leu Ser Leu Leu Ser Ile Ile Val
416 225          230          235          240
419 Leu Val Leu Val Lys Glu Leu Asn Glu Gln Phe Lys Arg Lys Ile Lys
420           245          250          255
423 Val Val Leu Pro Val Asp Leu Val Leu Ile Ile Ala Ala Ser Phe Ala
424           260          265          270
427 Cys Tyr Cys Thr Asn Met Glu Asn Thr Tyr Gly Leu Glu Val Val Gly
428           275          280          285
431 His Ile Pro Asn Gly Ile Pro Pro Pro Arg Ala Pro Pro Met Asn Ile
432           290          295          300
435 Leu Ser Ala Val Leu Thr Glu Ala Phe Gly Val Ala Leu Val Gly Tyr
436 305          310          315          320
439 Val Ala Ser Leu Ala Leu Ala Gln Gly Ser Ala Lys Lys Phe Lys Tyr
440           325          330          335
443 Ser Val Asp Asp Asn Gln Glu Phe Leu Ala His Gly Leu Ser Asn Val
444           340          345          350
447 Ile Pro Ser Phe Leu Phe Cys Ile Pro Ser Ala Ala Ala Met Gly Arg
448           355          360          365
451 Thr Ala Gly Leu Tyr Ser Thr Gly Ala Lys Thr Gln Val Ala Cys Leu
452           370          375          380
455 Ile Ser Cys Ile Phe Val Leu Ile Val Ile Tyr Ala Ile Gly Pro Leu
456 385          390          395          400

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date